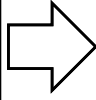
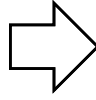


100 bp paired end sequencing
of 3 normalized hydractinia polyp
libraries. Multiplexed in 3 lanes.



dactylozooid: 554,807,328 pe reads
gastrozooid: 518,063,156 pe reads
gonozooids: 793,939,412 pe reads



CLC: Raw reads pooled for all polyps
and assembled into ~96,000 contigs

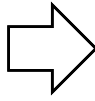
Annotation

Reciprocal Blast

tblastx

OrthoMCL Orthology database
Genomes: 150
Protein Sequences: 1,398,546
Ortholog Groups: 124,740

blastx



Py Scripts: Check top 10 hits, with
e-value ≥ 0.0001 , for each blast
search

if hits
reciprocal

if hits
annotated

if hits not
annotated

Blast against nr.

Get GO terms.

if hits
annotated

1



GORetriever on AgBase

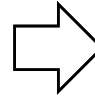
Functional Annotation
on David

2

Differential Expression

Bowtie2: Raw reads
mapped to CLC contigs
for each polyp.

Py Script: Mapped read counts
extracted from sorted sam files.
Reads counted as mapped if:
1. Both pairs map to the same scaffold
2. Neither pair was sequenced as all N's



1

DeSeq: 2 mouthless polyps
treated as biological
replicates and compared to
polyp with mouth.

2

Py Script: Mapped read counts
compared between polyps to
extract genes with $\geq 90\%$
up or down regulation.

3

Py Script (Steve): Bootstrap
distributions created to test for
significant de between polyps.